167-30075



WOODS HOLD OCEANOGRAPHIC INST. NSR-22-014-001

SEPARATION OF PROTEINS IN MOLLUSC SHELLS BY GEL-FILTRATION

Proteins and glycoproteins are involved in biological mineralization processes. For example, collagens in bone structures of vertebrates promote the formation of apatite seeds $\frac{1}{2}$, whereas glycoproteins in the exoskeleton of crabs provide a set of highly specific templates for calcite nucleation $\frac{2}{}$. In molluscs, a wide, array of structurally different proteins are contained in the shell structures, attesting to the heterogenity of calcified tissues $\frac{3}{2}$.

It has been suggested that independent of the kind of protein participating in crystal-seed formation, the most essential factor, in nucleating a mineral phase appears to be the availability of free carboxyl groups provided by certain acidic amino acids and free amino groups by certain basic amino acids and hexosamines $\frac{1-4}{2}$. It is thus inferred that throughout the animal kingdom, Nature adheres to the same principles when it comes to the formation of mineral nuclei.

To test this assumption, mollusc shell tissues of widely different biochemical composition and phylogeny have been studied by means of enzymatic and non-enzymatic degradation techniques and by gel-filtration. Tryptic digests did not result in the dissolution of shell matrix proteins but treatments with urea, hydroxylamine and formic acid degraded the tissues. According to preliminary studies, the hydroxylamine treatment resulted in a cleavage of the protein molecule to units of molecular weight of approximately 20,000 to $80,000\frac{4}{}$

The analytical scheme followed during the present investigation is outlined in Figure 1. The decalcified organic tissue was treated with a

hydroxylamine/6 M Urea solution for 24 hours at 45°C and subsequently with 95% formic acid for 4 hours at 45°C. Each treatment was followed by centrifugation and by gel-filtration of the supernatent, on G-25 Sephadex columns.

A variety of buffer systems were tested and the molality of the buffers (0.1 to 1) did not play a significant role in the efficiency of separation. Although some buffer systems proved to be slightly better than the routinely used borax buffer of pH 9 (hydroxylamine/urea fraction) and formic acid buffer of pH 3.0 (formic acid fraction) the two latter ones interfered least with the subsequent amino acid analysis. The high-molecular fractions (M.W.>5.000) were hydrolyzed and examined for their amino acid composition—. To facilitate a comparison, the amino acid analysis of the original samples and the residues are included in Table 1.

The analytical data indicate that throughout the molluscan phylum the urea/hydroxylamine fraction is consistently enriched in aspartic acid, lysine and amino sugars although this relationship is not necessarily displayed when these three amino compounds are highly concentrated in the original shell. It is tentatively suggested that this peptide fraction contains the active sites for the deposition of the mineral phase and that the remaining part of the proteinaceous matrix in the shells is not involved in the actual calcification. It is reasonable to assume that similar structures are contained in other mineralized tissues such as are found in bones or teeth. A full account on the phylogenetic and chemical aspects of these experiments will be presented elsewhere, together with several hundred amino acid analyses from calcified and uncalcified proteins 5/.

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- 6. The work was sponsored by the National Aeronautics and Space Administration and by a grant from the Petroleum Research Fund administered by the American Chemical Society. Contribution No. 1961 from the Woods Hole Oceanographic Institution.

Figure 1 Flow diagram of analytical procedures

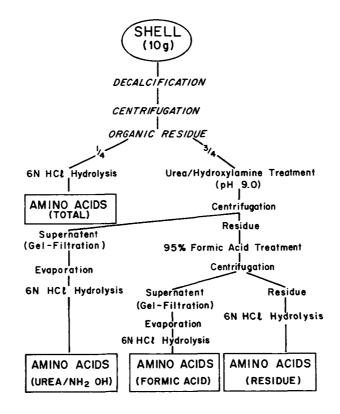


TABLE 1 A

AMINO ACID COMPOSITION OF MOLLUSC SHELL PROTEINS AND ISOLATED PEPTIDE/PROTEIN FRACTIONS - (IN RESIDUES PER 1000)

CRYPTOCHITON A/ FORMIC F (2)
7. [7
68 77 113
88
29
7 4 0 87 121
٥.٥
2.24

* Number in parentheses indicate the number of individual analyses.

TABLE 1 B

AMINO ACID COMPOSITION OF MOLLUSC SHELL PROTEINS AND ISOLATED PEPTIDE/PROTEIN FRACTIONS - (IN RESIDUES PER 1000)

	RESIDUE	(1)	101	23	69	%1	29	138	45	&	78	æ	4	74	01	Ξ		41	10	78		250	
LAEVICARDIUM	FORMIC	(1)	14	78	127	53	8	227	81	26	16	_	•	54	15	53		31	16	12		48	
₽	TOTAL UREA/	(4)	125	22	58	8	87	195	88	%	26	25	31	4	17	20		24	'n	10		179	0.54
	RESIDUE	(2)	115	46	62	22	911	248	72	24	34	14	23	35	53	33		36	ო	30		128	
MERCENARIA	FORMIC	(1)	187	47	52	አ	126	103	1	12	35	ო	22	4	34	32		75	٥	42		85	
MERC	UREA/ NH2OH	(3)	196	24	102	8	16	133	22	77	35	12	77	35	4	53		69	22	54		45	_
	TOTAL	4	148	47	72	7	128	146	2	71	32	7	77	35	45	æ		8	Ŋ	4		102	0.28
	RESIDUE	(1)	245	30	143	છ	36	228	55	20	37	-	21	31	12	13		43	٥	12		n.d.	
AE QUIPECTEN	FORMIC																						
AEGL	UREA/ NH2OH	Ξ	340	15	218	22	12	211	4	٥	5	-	œ	16	4	9	-	g	S	ო		19	ю
	TOTAL	<u>4</u>	296	38	186	26	23	214	62	15	81	9	15	52	5	∞	-	56	က	∞		118	0.25
	RESIDUE	(2)	72	18	84	32	16	367	205	2	8	9	18	20	35	15		10	-	14		752	
MYTILUS	FORMIC	Ξ	118	17	8	4	15	293	216	13	53	9	18	84	5	17		81	Ŋ	24		856	
W	UREA/ NH2OH	(2)	159	26	8	8	82	226	8	13	36	٥	74	25	13	91		\$	7	12		37	
	TOTAL	(5)	95	19	ಜ	38	8	357	83	13	22	7	15	4	34	15		7	4	19		394	0.91
			ASPARTIC ACID	THREONINE	SERINE	GLUTAMIC ACID	PROLINE	GLYCINE	ALANINE	CYSTINE	VALINE	METHIONINE	ISOLEUCINE	LEUCINE	TYROSINE	PHENYLALANINE	OH - LYSINE	LYSINE	HISTIDINE	ARGININE	PROTEIN	HEXOSAMINES	PERCENT PROTEIN IN TOTAL SHELL

* Number in parentheses indicate the number of individual analyses.